

Claims

1. DNA sequences which contain the coding region of an amino acid transporter, characterised in that the information contained in the nucleotide sequence allows, by integration in a plant genome, the formation of RNA, and with this RNA, a new amino acid transport activity can be introduced in the plant cells or an endogenous amino acid transporter activity can be expressed.
2. A DNA sequence according to claim 1, characterised in that, it contains the following nucleotide sequence (Seq-ID No 1):

CTTAAACAT TTATTTATC TTCTTCTTGT TCTCTCTTTC TCTTTCTCTC ATCACT 56

ATG AAG AGT TTC AAC ACA GAA GGA CAC AAC CAC TCC ACG GCG GAA 101
Met Lys Ser Phe Asn Thr Glu Gly His Asn His Ser Thr Ala Glu
1 5 10 15

TCC GGC GAT GCC TAC ACC GTG TCG GAC CCG ACA AAG AAC GTC GAT 146
Ser Gly Asp Ala Tyr Thr Val Ser Asp Pro Thr Lys Asn Val Asp
20 25 30

GAA GAT GGT CGA GAG AAG CGT ACC GGG ACG TGG CTT ACG GCG AGT 191
Glu Asp Gly Arg Glu Lys Arg Thr Gly Thr Trp Leu Thr Ala Ser
35 40 45

GCG CAT ATT ATC ACG GCG GTG ATA GCC TCC GGA GTG TTG TCT TTA 236
Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu
50 55 60

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GCA TGG GCT ATA GCT CAG CTT GGT TGG ATC GCA GGG ACA TCG ATC 281
 Ala Trp Ala Ile Ala Gln Leu Gly Trp Ile Ala Gly Thr Ser Ile
 65 70 75

TTA CTC ATT TTC TCG TTC ATT ACT TAC TTC ACC TCC ACC ATG CTT 326
 Leu Leu Ile Phe Ser Phe Ile Thr Tyr Phe Thr Ser Thr Met Leu
 80 85 90

GCC GAT TGC TAC CGT GCG CCG GAT CCC GTC ACC GGA AAA CGG AAT 371
 Ala Asp Cys Tyr Arg Ala Pro Asp Pro Val Thr Gly Lys Arg Asn
 95 100 105

TAC ACT TAC ATG GAC GTT GTT CGA TCT TAC CTC GGT GGT AGG AAA 416
 Tyr Thr Tyr Met Asp Val Val Arg Ser Tyr Leu Gly Gly Arg Lys
 110 115 120

GTG CAG CTC TGT GGA GTG GCA CAA TAT GGG AAT CTG ATT GGG GTC 461
 Val Gln Leu Cys Gly Val Ala Gln Tyr Gly Asn Leu Ile Gly Val
 125 130 135

ACT GTT GGT TAC ACC ATC ACT GCT TCT ATT AGT TTG GTA GCG GTA 506
 Thr Val Gly Tyr Thr Ile Thr Ala Ser Ile Ser Leu Val Ala Val
 140 145 150

GGG AAA TCG AAC TGC TTC CAC GAT AAA GGG CAC ACT GCG GAT TGT 551
 Gly Lys Ser Asn Cys Phe His Asp Lys Gly His Thr Ala Asp Cys
 155 160 165

ACT ATA TCG AAT TAT CCG TAT ATG GCG GTT TTT GGT ATC ATT CAA 596
 Thr Ile Ser Asn Tyr Pro Tyr Met Ala Val Phe Gly Ile Ile Gln
 170 175 180

GTT ATT CTT AGC CAG ATC CCA AAT TTC CAC AAG CTC TCT TTT CTT 641
 Val Ile Leu Ser Gln Ile Pro Asn Phe His Lys Leu Ser Phe Leu
 185 190 195

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TCC ATT ATG GCC GCA GTC ATG TCC TTT ACT TAT GCA ACT ATT GGA 686
 Ser Ile Met Ala Ala Val Met Ser Phe Thr Tyr Ala Thr Ile Gly
 200 205 210

ATC GGT CTA GCC ATC GCA ACC GTC GCA GGT GGG AAA GTG GGT AAG 731
 Ile Gly Leu Ala Ile Ala Thr Val Ala Gly Gly Lys Val Gly Lys
 215 220 225

ACG AGT ATG ACG GGC ACA GCG GTT GGA GTA GAT GTA ACC GCA GCT 776
 Thr Ser Met Thr Gly Thr Ala Val Gly Val Asp Val Thr Ala Ala
 230 235 240

CAA AAG ATA TGG AGA TCG TTT CAA GCG GTT GGG GAC ATA GCG TTC 821
 Gln Lys Ile Trp Arg Ser Phe Gln Ala Val Gly Asp Ile Ala Phe
 245 250 255

GCC TAT GCT TAT GCC ACG GTT CTC ATC GAG ATT CAG GAT ACA CTA 866
 Ala Tyr Ala Tyr Ala Thr Val Leu Ile Glu Ile Gln Asp Thr Leu
 260 265 270

AGA TCT AGC CCA GCT GAG AAC AAA GCC ATG AAA AGA GCA AGT CTT 911
 Arg Ser Ser Pro Ala Glu Asn Lys Ala Met Lys Arg Ala Ser Leu
 275 280 285

GTG GGA GTA TCA ACC ACC ACT TTT TTC TAC ATC TTA TGT GGA TGC 956
 Val Gly Val Ser Thr Thr Thr Phe Phe Tyr Ile Leu Cys Gly Cys
 290 295 300

ATC GGC TAT GCT GCA TTT GGA AAC AAT GCC CCT GGA GAT TTC CTC 1001
 Ile Gly Tyr Ala Ala Phe Gly Asn Asn Ala Pro Gly Asp Phe Leu
 305 310 315

ACA GAT TTC GGG TTT TTC GAG CCC TTT TGG CTC ATT GAC TTT GCA 1046
 Thr Asp Phe Gly Phe Phe Glu Pro Phe Trp Leu Ile Asp Phe Ala
 320 325 330

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AAC GCT TGC ATC GCT GTC CAC CTT ATT GGT GCC TAT CAG GTG TTC 1091
 Asn Ala Cys Ile Ala Val His Leu Ile Gly Ala Tyr Gln Val Phe
 335 340 345

GCG CAG CCG ATA TTC CAG TTT GTT GAG AAA AAA TGC AAC AGA AAC 1136
 Ala Gln Pro Ile Phe Gln Phe Val Glu Lys Lys Cys Asn Arg Asn
 350 355 360

TAT CCA GAC AAC AAG TTC ATC ACT TCT GAA TAT TCA GTA AAC GTA 1181
 Tyr Pro Asp Asn Lys Phe Ile Thr Ser Glu Tyr Ser Val Asn Val
 365 370 375

CCT TTC CTT GGA AAA TTC AAC ATT AGC CTC TTC AGA TTG GTG TGG 1226
 Pro Phe Leu Gly Lys Phe Asn Ile Ser Leu Phe Arg Leu Val Trp
 380 385 390

AGG ACA GCT TAT GTG GTT ATA ACC ACT GTT GTA GCT ATG ATA TTC 1271
 Arg Thr Ala Tyr Val Val Ile Thr Thr Val Val Ala Met Ile Phe
 395 400 405

CCT TTC TTC AAC GCG ATC TTA GGT CTT ATC GGA GCA GCT TCC TTC 1316
 Pro Phe Phe Asn Ala Ile Leu Gly Leu Ile Gly Ala Ala Ser Phe
 410 415 420

TGG CCT TTA ACG GTT TAT TTC CCT GTG GAG ATG CAC ATT GCA CAA 1361
 Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met His Ile Ala Gln
 425 430 435

ACC AAG ATT AAG AAG TAC TCT GCT AGA TGG ATT GCG CTG AAA ACG 1406
 Thr Lys Ile Lys Lys Tyr Ser Ala Arg Trp Ile Ala Leu Lys Thr
 440 445 450

ATG TGC TAT GTT TGC TTG ATC GTC TCG CTC TTA GCT GCA GCC GGA 1451
 Met Cys Tyr Val Cys Leu Ile Val Ser Leu Leu Ala Ala Ala Gly
 455 460 465

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TCC ATC GCA GGA CTT ATA AGT AGT GTC AAA ACC TAC AAG CCC TTC 1496
 Ser Ile Ala Gly Leu Ile Ser Ser Val Lys Thr Tyr Lys Pro Phe
 470 475 480

CGG ACT ATG CAT GAG TGAGTTTGAG ATCCTCAAGA GAGTCAAAAA 1541
 Arg Thr Met His Glu
 485

TATATGTAGT AGTTTGGTCT TTCTGTTAAA CTATCTGGTG TCTAAATCCA 1591

ATGAGAATGC TTTATTGCTA AACTTCATG AATCTCTCTG TATCTACATC 1641

TTTCAATCTA ATACATATGA GCTCTTCCAA AAAAAAAAAA AAAA 1685

3. A DNA sequence according to claim 1, characterised in that it contains the following nucleotide sequence (Seq-ID No 2):

CTATTTTAT AATTCCTCTT CTTTTTGTTT 29

ATAGCTTTGT AATTATAGTC TTATTCTCT TTAAGGCTCA ATAAGAGGAG 79

ATG GGT GAA ACC GCT GCC GCC AAT AAC CAC CGT CAC CAC CAC CAT 124
 Met Gly Glu Thr Ala Ala Ala Asn Asn His Arg His His His His
 1 5 10 15

CAC GGC CAC CAG GTC TTT GAC GTG GCC AGC CAC GAT TTC GTC CCT 169
 His Gly His Gln Val Phe Asp Val Ala Ser His Asp Phe Val Pro
 20 25 30

CCA CAA CCG GCT TTT AAA TGC TTC GAT GAT GAT GGC CGC CTC AAA 214
 Pro Gln Pro Ala Phe Lys Cys Phe Asp Asp Asp Gly Arg Leu Lys
 35 40 45

AGA ACT GGG ACT GTT TGG ACC GCG AGC GCT CAT ATA ATA ACT GCG 259
 Arg Thr Gly Thr Val Trp Thr Ala Ser Ala His Ile Ile Thr Ala
 50 55 60

GTT ATC GGA TCC GGC GTT TTG TCA TTG GCG TGG GCG ATT GCA CAG 304
 Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln
 65 70 75

CTC GGA TGG ATC GCT GGC CCT GCT GTG ATG CTA TTG TTC TCT CTT 349
 Leu Gly Trp Ile Ala Gly Pro Ala Val Met Leu Leu Phe Ser Leu
 80 85 90

GTT ACT CTT TAC TCC TCC ACA CTT CTT AGC GAC TGC TAC AGA ACC 394
 Val Thr Leu Tyr Ser Ser Thr Leu Leu Ser Asp Cys Tyr Arg Thr
 95 100 105

GGC GAT GCA GTG TCT GGC AAG AGA AAC TAC ACT TAC ATG GAT GCC 439
 Gly Asp Ala Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala
 110 115 120

GTT CGA TCA ATT CTC GGT GGG TTC AAG TTC AAG ATT TGT GGG TTG 484
 Val Arg Ser Ile Leu Gly Gly Phe Lys Phe Lys Ile Cys Gly Leu
 125 130 135

ATT CAA TAC TTG AAT CTC TTT GGT ATC GCA ATT GGA TAC ACG ATA 529
 Ile Gln Tyr Leu Asn Leu Phe Gly Ile Ala Ile Gly Tyr Thr Ile
 140 145 150

GCA GCT TCC ATA AGC ATG ATG GCG ATC AAG AGA TCC AAC TGC TTC 574
 Ala Ala Ser Ile Ser Met Met Ala Ile Lys Arg Ser Asn Cys Phe
 155 160 165

CAC AAG AGT GGA GGA AAA GAC CCA TGT CAC ATG TCC AGT AAT CCT 619
 His Lys Ser Gly Gly Lys Asp Pro Cys His Met Ser Ser Asn Pro
 170 175 180

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TAC ATG ATC GTA TTT GGT GTG GCA GAG ATC TTG CTC TCT CAG GTT 664
 Tyr Met Ile Val Phe Gly Val Ala Glu Ile Leu Leu Ser Gln Val
 185 190 200

CCT GAT TTC GAT CAG ATT TGG TGG ATC TCC ATT GTT GCA GCT GTT 709
 Pro Asp Phe Asp Gln Ile Trp Trp Ile Ser Ile Val Ala Ala Val
 205 210 220

ATG TCC TTC ACT TAC TCT GCC ATT GGT CTA GCT CTT GGA ATC GTT 754
 Met Ser Phe Thr Tyr Ser Ala Ile Gly Leu Ala Leu Gly Ile Val
 225 230 235

CAA GTT GCA GCG AAT GGA GTT TTC AAA GGA AGT CTC ACT GGA ATA 799
 Gln Val Ala Ala Asn Gly Val Phe Lys Gly Ser Leu Thr Gly Ile
 240 245 250

AGC ATC GGA ACA GTG ACT CAA ACA CAG AAG ATA TGG AGA ACC TTC 844
 Ser Ile Gly Thr Val Thr Gln Thr Gln Lys Ile Trp Arg Thr Phe
 255 260 265

CAA GCA CTT GGA GAC ATT GCC TTT GCG TAC TCA TAC TCT GTT GTC 889
 Gln Ala Leu Gly Asp Ile Ala Phe Ala Tyr Ser Tyr Ser Val Val
 270 275 280

CTA ATC GAG ATT CAG GAT ACT GTA AGA TCC CCA CCG GCG GAA TCG 934
 Leu Ile Glu Ile Gln Asp Thr Val Arg Ser Pro Pro Ala Glu Ser
 285 290 295

AAA ACG ATG AAG AAA GCA ACA AAA ATC AGT ATT GCC GTC ACA ACT 979
 Lys Thr Met Lys Lys Ala Thr Lys Ile Ser Ile Ala Val Thr Thr
 300 305 310

ATC TTC TAC ATG CTA TGT GGC TCA ATG GGT TAT GCC GCT TTT GGA 1024
 Ile Phe Tyr Met Leu Cys Gly Ser Met Gly Tyr Ala Ala Phe Gly
 315 320 325

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GAT GCA GCA CCG GGA AAC CTC CTC ACC GGT TTT GGA TTC TAC AAC 1069
 Asp Ala Ala Pro Gly Asn Leu Leu Thr Gly Phe Gly Phe Tyr Asn
 330 335 340

CCG TTT TGG CTC CTT GAC ATA GCT AAC GCC GCC ATT GTT GTC CAC 1114
 Pro Phe Trp Leu Leu Asp Ile Ala Asn Ala Ala Ile Val Val His
 245 350 355

CTC GTT GGA GCT TAC CAA GTC TTT GCT CAG CCC ATC TTT GCC TTT 1159
 Leu Val Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Ala Phe
 360 365 370

ATT GAA AAA TCA GTC GCA GAG AGA TAT CCA GAC AAT GAC TTC CTC 1204
 Ile Glu Lys Ser Val Ala Glu Arg Tyr Pro Asp Asn Asp Phe Leu
 375 380 385

AGC AAG GAA TTT GAA ATC AGA ATC CCC GGA TTT AAG TCT CCT TAC 1249
 Ser Lys Glu Phe Glu Ile Arg Ile Pro Gly Phe Lys Ser Pro Tyr
 390 395 400

AAA GTA AAC GTT TTC AGG ATG GTP TAC AGG AGT GGC TTT GTC GTT 1294
 Lys Val Asn Val Phe Arg Met Val Tyr Arg Ser Gly Phe Val Val
 405 410 415

ACA ACC ACC GTG ATA TCG ATG CTG ATG CCG TTT TTT AAC GAC GTG 1339
 Thr Thr Thr Val Ile Ser Met Leu Met Pro Phe Phe Asn Asp Val
 420 425 430

GTC GGG ATC TTA GGG GCG TTA GGG TTT TGG CCC TTG ACG GTT TAT 1384
 Val Gly Ile Leu Gly Ala Leu Gly Phe Trp Pro Leu Thr Val Tyr
 435 440 445

TTT CCG GTG GAG ATG TAT ATT AAG CAG AGG AAG GTT GAG AAA TGG 1429
 Phe Pro Val Glu Met Tyr Ile Lys Gln Arg Lys Val Glu Lys Trp
 450 455 460

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AGC ACG AGA TGG GTG TGT TTA CAG ATG CTT AGT GTT GCT TGT CTT 1474
 Ser Thr Arg Trp Val Cys Leu Gln Met Leu Ser Val Ala Cys Leu
 465 470 475

GTG ATC TCG GTG GTC GCC GGG GTT GGA TCA ATC GCC GGA GTG ATG 1519
 Val Ile Ser Val Val Ala Gly Val Gly Ser Ile Ala Gly Val Met
 480 485 490

CTT GAT CTT AAG GTC TAT AAG CCA TTC AAG TCT ACA TAT 1558
 Leu Asp Leu Lys Val Tyr Lys Pro Phe Lys Ser Thr Tyr
 495 500

TGATGATTAT GGACCATGAA CAACAGAGAG AGTTGGTGTG TAAAGTTTAC 1608

CATTCAAAG AAAACTCCAA AAATGTGTAT ATTGTATGTT GTTCTCATT 1658

CGTATGGTCT CATCTTTGTA ATAAAATTTA AAACCTATGT TATAAATTAT 1708

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 1740

4. A plasmid, characterised in that it contains a DNA sequence according to any one of claims 1 to 3.
5. Plasmid pPPP1-20 (DSM 7129).
6. Plasmid pAAP2, prepared according to Example 2.
7. Plasmid pBin PPP1-20 (DSM 7130).
- 10 8. Use of the plasmid according to any one of claims 4 to 7 or derivatives or parts thereof, for the transformation of prokaryotic and eukaryotic cells.
- 15 9. Plants containing a DNA sequence according to any one of claims 1 to 3.

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10. Bacteria containing a DNA sequence according to any one of claims 1 to 3.
- 5 11. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the preparation of plasmids with changed specificity of the transporter.
- 10 12. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for isolation of similar sequences from the genome of the plant.
- 15 13. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the expression of translatable mRNA, that makes possible the synthesis of an amino acid transporter in prokaryotic and eukaryotic cells.
- 20 14. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the expression of a non-translatable mRNA, that hinders the synthesis of an amino acid transporter in prokaryotic and eukaryotic cells.
- 25 15. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 in combination with steering elements for an expression in prokaryotic and eukaryotic cells.
- 30 16. Yeast strains containing DNA sequences according to any one of claims 1 to 3.
- 35 17. Use of yeast strains containing DNA sequences according to claim 16 for identification of a plant amino acid transporter.

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18. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for preparation of plants with changed amino acid and nitrogen metabolism.

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19. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for preparation of crop plants with increased yield.

10 20. Use of the DNA sequence of the amino acid transporter according to any one of claims 1 to 3 for the transport of compounds in prokaryotic and eukaryotic cells.

Add
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